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#8



RAW SEQUENCE LISTING

DATE: 07/30/2002

PATENT APPLICATION: US/09/887,853

TIME: 14:22:01

Input Set : N:\Crf3\RULE60\09887853.raw

Output Set: N:\CRF3\07302002\I887853.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Huston, James S.

6 Oppermann, Hermann

7 Houston, L. L.

8 Ring, David B.

10 (ii) TITLE OF INVENTION: Biosynthetic Binding Proteins For

11 Imaging

13 (iii) NUMBER OF SEQUENCES: 11

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department

17 (B) STREET: Exchange Place, 53 State Street

18 (C) CITY: Boston

19 (D) STATE: Massachusetts

20 (E) COUNTRY: USA

21 (F) ZIP: 02109

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/887,853

C--> 31 (B) FILING DATE: 21-Jun-2001

32 (C) CLASSIFICATION:

36 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: US/08/133,804

38 (B) FILING DATE:

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Kelley, Robin D.

44 (B) REGISTRATION NUMBER: 34,637

45 (C) REFERENCE/DOCKET NUMBER: 2054/22

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 617-248-7477

49 (B) TELEFAX: 617-248-7100

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 909 base pairs

56 (B) TYPE: nucleic acid

57 (C) STRANDEDNESS: single

58 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: cDNA

63 (ix) FEATURE:

ENTERED

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64      (A) NAME/KEY: CDS
65      (B) LOCATION: 3..752
66      (D) OTHER INFORMATION: /product= "741F8 sFv' C-terminal
67 Gly4-Cys"
69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72 CC ATG GCG GAG ATC CAA TTG GTG CAG TCT GGA CCT GAG CTG AAG AAG      47
73 Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
74      1          5          10          15
76 CCT GGA GAG ACA GTC AAG ATC TCC TGC AAG GCT TCT GGG TAT ACC TTC      95
77 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
78      20          25          30
80 ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG GCT CCA GGA AAG GGT TTA      143
81 Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
82      35          40          45
84 AAG TGG ATG GGC TGG ATA AAC ACC AAC ACT GGA GAG CCA ACA TAT GCT      191
85 Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala
86      50          55          60
88 GAA GAG TTC AAG GGA CGG TTT GCC TTC TCT TTG GAA ACC TCT GCC AGC      239
89 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
90      65          70          75
92 ACT GCC TAT TTG CAG ATC AAC AAC CTC AAA AAT GAG GAC ACG GCT ACA      287
93 Thr Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr
94      80          85          90
96 TAT TTC TGT GGA AGG CAA TTT ATT ACC TAC GGC GGG TTT GCT AAC TGG      335
97 Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp
98      100         105         110
100 GGC CAA GGG ACT CTG GTC ACT GTC TCT GCA TCG AGC TCC TCC GGA TCT      383
101 Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Gly Ser
102      115         120         125
104 TCA TCT AGC GGT TCC AGC TCG AGC GAT ATC GTC ATG ACC CAG TCT CCT      431
105 Ser Ser Ser Gly Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro
106      130         135         140
108 AAA TTC ATG TCC ACG TCA GTG GGA GAC AGG GTC AGC ATC TCC TGC AAG      479
109 Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys
110      145         150         155
112 GCC AGT CAG GAT GTG AGT ACT GCT GTA GCC TGG TAT CAA CAA AAA CCA      527
113 Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
114      160         165         170
116 GGG CAA TCT CCT AAA CTA CTG ATT TAC TGG ACA TCC ACC CGG CAC ACT      575
117 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr
118      180         185         190
120 GGA GTC CCT GAT CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TAT ACT      623
121 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr
122      195         200         205
124 CTC ACC ATC AGC AGT GTG CAG GCT GAA GAC CTG GCA CTT CAT TAC TGT      671
125 Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys
126      210         215         220
128 CAG CAA CAT TAT AGA GTG CCG TAC ACG TTC GGA GGG ACC AAG CTG      719
129 Gln Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Thr Lys Leu

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130      225      230      235
132 GAG ATA AAA CGG GCT GAT GGG GGA GGT GGA TGT TAACGGGGGA GGTGGATGTT      772
133 Glu Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys
134 240      245      250
136 GGGTCTCGTT ACGTTGCGGA TCTCGAGGCT ATCTTTACTA ACTCTTACCG TAAAGTTCTG      832
138 GCTCAACTGT CTGCACGCAA GCTTTTGACG GATATCATGA GCGCTTAAGA TCCGTGCGACC      892
140 TGCAGGCATG CAAGCTT      909
143 (2) INFORMATION FOR SEQ ID NO: 2:
145 (i) SEQUENCE CHARACTERISTICS:
146 (A) LENGTH: 250 amino acids
147 (B) TYPE: amino acid
148 (D) TOPOLOGY: linear
150 (ii) MOLECULE TYPE: protein
152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
154 Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
155 1      5      10      15
157 Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
158      20      25      30
160 Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys
161      35      40      45
163 Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu
164      50      55      60
166 Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr
167 65      70      75      80
169 Ala Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr
170      85      90      95
172 Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly
173      100      105      110
175 Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser
176      115      120      125
178 Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys
179      130      135      140
181 Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala
182 145      150      155      160
184 Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
185      165      170      175
187 Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
188      180      185      190
190 Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
191      195      200      205
193 Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln
194      210      215      220
196 Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
197 225      230      235      240
199 Ile Lys Arg Ala Asp Gly Gly Gly Cys
200      245      250
202 (2) INFORMATION FOR SEQ ID NO: 3:
204 (i) SEQUENCE CHARACTERISTICS:
205 (A) LENGTH: 779 base pairs

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206      (B) TYPE: nucleic acid
207      (C) STRANDEDNESS: single
208      (D) TOPOLOGY: linear
210      (ii) MOLECULE TYPE: cDNA
213      (ix) FEATURE:
214          (A) NAME/KEY: CDS
215          (B) LOCATION: 3..758
216          (D) OTHER INFORMATION: /product= "26-10 sFv" with
217 C-terminal Gly4-Cys"
220      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
222 CC ATG GAA GTT CAA CTG CAA CAG TCT GGT CCT GAA TTG GTT AAA CCT      47
223   Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro
224     1         5         10        15
226 GGC GCC TCT GTG CGC ATG TCC TGC AAA TCC TCT GGG TAC ATT TTC ACC      95
227 Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr
228     20        25        30
230 GAC TTC TAC ATG AAT TGG GTT CGC CAG TCT CAT GGT AAG TCT CTA GAC      143
231 Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp
232     35        40        45
234 TAC ATC GGG TAC ATT TCC CCA TAC TCT GGT ACC GGC TAC AAC CAG      191
235 Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln
236     50        55        60
238 AAG TTT AAA GGT AAG GCG ACC CTT ACT GTC GAC AAA TCT TCC TCA ACT      239
239 Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
240     65        70        75
242 GCT TAC ATG GAG CTG CGT TCT TTG ACC TCT GAG GAC TCC GCG GTA TAC      287
243 Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
244     80        85        90        95
246 TAT TGC GCG GGC TCC TCT GGT AAC AAA TGG GCC ATG GAT TAT TGG GGT      335
247 Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly
248    100       105       110
250 CAT GGT GCT AGC GTT ACT GTG AGC TCC TCC GGA TCT TCA TCT AGC GGT      383
251 His Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly
252    115       120       125
254 TCC AGC TCG AGT GGA TCC GAC GTC GTA ATG ACC CAG ACT CCG CTG TCT      431
255 Ser Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser
256    130       135       140
258 CTG CCG GTT TCT CTG GGT GAC CAG GCT TCT ATT TCT TGC CGC TCT TCC      479
259 Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
260    145       150       155
262 CAG TCT CTG GTC CAT TCT AAT GGT AAC ACT TAC CTG AAC TGG TAC CTG      527
263 Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu
264    160       165       170       175
266 CAA AAG GCT GGT CAG TCT CCG AAG CTT CTG ATC TAC AAA GTC TCT AAC      575
267 Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn
268    180       185       190
270 CGC TTC TCT GGT GTC CCG GAT CGT TTC TCT GGT TCT GGT TCT GGT ACT      623
271 Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
272    195       200       205

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274 GAC TTC ACC CTG AAG ATC TCT CGT GTC GAG GCC GAA GAC CTG GGT ATC      671
275 Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile
276          210          215          220
278 TAC TTC TGC TCT CAG ACT ACT CAT GTA CCG CCG ACT TTT GGT GGT GGC      719
279 Tyr Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly
280          225          230          235
282 ACC AAG CTC GAG ATT AAA CGT TCC GGG GGA GGT GGA TGT TAACTGCAGC      768
283 Thr Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Cys
284 240          245          250
286 CCGGGGGATC C      779
289 (2) INFORMATION FOR SEQ ID NO: 4:
291 (i) SEQUENCE CHARACTERISTICS:
292 (A) LENGTH: 252 amino acids
293 (B) TYPE: amino acid
294 (D) TOPOLOGY: linear
296 (ii) MOLECULE TYPE: protein
298 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
300 Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
301 1          5          10          15
303 Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp
304          20          25          30
306 Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr
307          35          40          45
309 Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys
310          50          55          60
312 Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
313 65          70          75          80
315 Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
316          85          90          95
318 Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His
319          100          105          110
321 Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser
322          115          120          125
324 Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
325          130          135          140
327 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
328 145          150          155          160
330 Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln
331          165          170          175
333 Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
334          180          185          190
336 Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
337          195          200          205
339 Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr
340          210          215          220
342 Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr
343 225          230          235          240
345 Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
346          245          250

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/30/2002
PATENT APPLICATION: US/09/887,853 TIME: 14:22:02

Input Set : N:\Crf3\RULE60\09887853.raw
Output Set: N:\CRF3\07302002\I887853.raw

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The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:2; Line(s) 202
Seq#:3; Line(s) 289
Seq#:4; Line(s) 348
Seq#:5; Line(s) 433
Seq#:6; Line(s) 492
Seq#:7; Line(s) 514
Seq#:8; Line(s) 536
Seq#:9; Line(s) 558
Seq#:10; Line(s) 581

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/887,853

DATE: 07/30/2002

TIME: 14:22:02

Input Set : N:\Crf3\RULE60\09887853.raw

Output Set: N:\CRF3\07302002\I887853.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]